P. Duffy

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: ST. GEORGE-HYSLOP, PETER H          ENTERED
 6                       ROMMENS, JOHANNA M
 7                       FRASER, PAUL E
 8
 9       (ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
10                 TO ALZHEIMER'S DISEASE
11
12      (iii) NUMBER OF SEQUENCES: 183
13
14       (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
16            (B) STREET: 600 South Avenue West
17            (C) CITY: Westfield
18            (D) STATE: New Jersey
19            (E) COUNTRY: U.S.A.
20            (F) ZIP: 07090
21
22        (v) COMPUTER READABLE FORM:
23            (A) MEDIUM TYPE: Floppy disk
24            (B) COMPUTER: IBM PC compatible
25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D) SOFTWARE: Microsoft Word, Version 6.0c
27
28       (vi) CURRENT APPLICATION DATA:
29            (A) APPLICATION NUMBER: US 08/509,359
30            (B) FILING DATE: 31-JUL-95
31            (C) CLASSIFICATION:
32
33     (viii) ATTORNEY/AGENT INFORMATION:
34            (A) NAME: Palisi, Thomas M.
35            (B) REGISTRATION NUMBER: 36629
36
37       (ix) TELECOMMUNICATION INFORMATION:
38            (A) TELEPHONE: (908) 654-5000
39            (B) TELEFAX: (908) 654-7866
40
41
42   (2) INFORMATION FOR SEQ ID NO:1:
43
44        (i) SEQUENCE CHARACTERISTICS:
45            (A) LENGTH: 2791 base pairs
46            (B) TYPE: nucleic acid
```

```
47              (C) STRANDEDNESS: single
48              (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: cDNA
51
52
53      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55   TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG      60
56
57   GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA     120
58
59   TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCCTTA GACAGCTTGG CCTGGAGGAG     180
60
61   AACACATGAA AGAAAGAACC TCAAGAGGCT TTGTTTTCTG TGAAACAGTA TTTCTATACA     240
62
63   GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT     300
64
65   GAGGACAACC ACCTGAGCAA TACTGTACGT AGCCAGAATG ACAATAGAGA ACGGCAGGAG     360
66
67   CACAACGACA GACGGAGCCT TGGCCACCCT GAGCCATTAT CTAATGGACG ACCCCAGGGT     420
68
69   AACTCCCGGC AGGTGGTGGA GCAAGATGAG GAAGAAGATG AGGAGCTGAC ATTGAAATAT     480
70
71   GGCGCCAAGC ATGTGATCAT GCTCTTTGTC CCTGTGACTC TCTGCATGGT GGTGGTCGTG     540
72
73   GCTACCATTA AGTCAGTCAG CTTTTATACC CGGAAGGATG GGCAGCTAAT CTATACCCCA     600
74
75   TTCACAGAAG ATACCGAGAC TGTGGGCCAG AGAGCCCTGC ACTCAATTCT GAATGCTGCC     660
76
77   ATCATGATCA GTGTCATTGT TGTCATGACT ATCCTCCTGG TGGTTCTGTA TAAATACAGG     720
78
79   TGCTATAAGG TCATCCATGC CTGGCTTATT ATATCATCTC TATTGTTGCT GTTCTTTTTT     780
80
81   TCATTCATTT ACTTGGGGGA AGTGTTTAAA ACCTATAACG TTGCTGTGGA CTACATTACT     840
82
83   GTTGCACTCC TGATCTGGAA TTTGGGTGTG GTGGGAATGA TTTCCATTCA CTGGAAAGGT     900
84
85   CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCCTCATGGC CCTGGTGTTT     960
86
87   ATCAAGTACC TCCCTGAATG GACTGCGTGG CTCATCTTGG CTGTGATTTC AGTATATGAT    1020
88
89   TTAGTGGCTG TTTTGTGTCC GAAAGGTCCA CTTCGTATGC TGGTTGAAAC AGCTCAGGAG    1080
90
91   AGAAATGAAA CGCTTTTTCC AGCTCTCATT TACTCCTCAA CAATGGTGTG GTTGGTGAAT    1140
92
93   ATGGCAGAAG GAGACCCGGA AGCTCAAAGG AGAGTATCCA AAAATTCCAA GTATAATGCA    1200
94
95   GAAAGCACAG AAAGGGAGTC ACAAGACACT GTTGCAGAGA ATGATGATGG CGGGTTCAGT    1260
96
97   GAGGAATGGG AAGCCCAGAG GGACAGTCAT CTAGGGCCTC ATCGCTCTAC ACCTGAGTCA    1320
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99   CGAGCTGCTG TCCAGGAACT TTCCAGCAGT ATCCTCGCTG GTGAAGACCC AGAGGAAAGG    1380
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INPUT SET: S29990.raw

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101    GGAGTAAAAC TTGGATTGGG AGATTTCATT TTCTACAGTG TTCTGGTTGG TAAAGCCTCA    1440
102
103    GCAACAGCCA GTGGAGACTG GAACACAACC ATAGCCTGTT TCGTAGCCAT ATTAATTGGT    1500
104
105    TTGTGCCTTA CATTATTACT CCTTGCCATT TTCAAGAAAG CATTGCCAGC TCTTCCAATC    1560
106
107    TCCATCACCT TTGGGCTTGT TTTCTACTTT GCCACAGATT ATCTTGTACA GCCTTTTATG    1620
108
109    GACCAATTAG CATTCCATCA ATTTTATATC TAGCATATTT GCGGTTAGAA TCCCATGGAT    1680
110
111    GTTTCTTCTT TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA    1740
112
113    TCTAACAAAG TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC    1800
114
115    ACCTTGCACT ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC    1860
116
117    ATCGCAGTGG ACTGTGTCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA    1920
118
119    GATATGATAG GCCCGGAAGT TGCTGTGCCC CATCAGCAGC TTGACGCGTG GTCACAGGAC    1980
120
121    GATTTCACTG ACACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG    2040
122
123    TTTAAACCAA ACGGAACTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT    2100
124
125    GTATTAACTG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC    2160
126
127    AGAATGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA    2220
128
129    CTCATCCTTT TTAAATGAGA CTTGTTTTCC CCTCTCTTTG AGTCAAGTCA AATATGTAGA    2280
130
131    TGCCTTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATTT    2340
132
133    CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTTAA CCTCAGGTTC    2400
134
135    CAAATTCAGT AAATTTTGGA AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA    2460
136
137    AGTCAAATTT GGATTTTCCA CCAAATTCTG AATTTGTAGA CATACTTGTA CGCTCACTTG    2520
138
139    CCCCAGATGC CTCCTCTGTC CTCATTCTTC TCTCCCACAC AAGCAGTCTT TTTCTACAGC    2580
140
141    CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCACTT ATTCTAGGGT CTTACTCTTT    2640
142
143    GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC    2700
144
145    CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG    2760
146
147    AAGCAAAAAA AAAAAAAAAA AAAAAAAAAA A                                    2791
148
149
150    (2) INFORMATION FOR SEQ ID NO:2:
151
152        (i) SEQUENCE CHARACTERISTICS:
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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/509,359B*

DATE: 11/23/98
TIME: 13:48:44

INPUT SET: S29990.raw

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153        (A) LENGTH: 467 amino acids
154        (B) TYPE: amino acid
155        (C) STRANDEDNESS: single
156        (D) TOPOLOGY: linear
157
158
159   (ii) MOLECULE TYPE: protein
160
161   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
162
163      Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
164      1               5                  10                  15
165
166      Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
167              20                  25                  30
168
169      Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
170              35                  40                  45
171
172      Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
173              50                  55                  60
174
175      Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
176      65                  70                  75                  80
177
178      His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
179                      85                  90                  95
180
181      Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
182              100                 105                 110
183
184      Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
185              115                 120                 125
186
187      Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
188              130                 135                 140
189
190      Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
191      145                 150                 155                 160
192
193      Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
194                      165                 170                 175
195
196      Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
197              180                 185                 190
198
199      Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
200              195                 200                 205
201
202      Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
203              210                 215                 220
204
205      Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
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INPUT SET: S29990.raw

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206        225                    230                    235                    240
207
208        Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
209                        245                    250                    255
210
211        Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
212                        260                    265                    270
213
214        Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
215                275                    280                    285
216
217        Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
218                290                    295                    300
219
220        Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
221        305                    310                    315                    320
222
223        Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
224                        325                    330                    335
225
226        Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
227                        340                    345                    350
228
229        Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
230                355                    360                    365
231
232        Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
233                370                    375                    380
234
235        Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
236        385                    390                    395                    400
237
238        Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
239                        405                    410                    415
240
241        Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
242                        420                    425                    430
243
244        Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
245                435                    440                    445
246
247        Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
248                450                    455                    460
249
250        Phe Tyr Ile
251        465
252
253
254
255
256   (2) INFORMATION FOR SEQ ID NO:3:
257
258        (i) SEQUENCE CHARACTERISTICS:
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/509,359B*

INPUT SET: S29990.raw

Line	Error	Original Text